# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/763,976*

Source: *1FWO*

Date Processed by STIC: *7/12/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand-Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

# Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/763,976_ |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 ____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering — The numbering under each $5^{th}$ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)  (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING                    DATE: 07/12/2004
PATENT APPLICATION:  US/10/763,976     TIME: 15:16:58

         Input Set : N:\FATIMA\10763976.txt
         Output Set: N:\CRF4\07122004\J763976.raw

     3 <110> APPLICANT: Harms, Jerome S.
     4         Splitter, Gary A.
     5         Eakle, Kurt A.
     6         Bremel, Robert D.
     8 <120> TITLE OF INVENTION: Inducible Protein Expression System
W-->  0 <130> FILE REFERENCE:
    10 <140> CURRENT APPLICATION NUMBER: US 10/763,976
C--> 11 <141> CURRENT FILING DATE: 2004-07-07
    13 <160> NUMBER OF SEQ ID NOS: 13

*[handwritten: pp 1-4]*

*[handwritten: Does Not Comply Corrected Diskette Needed]*

ERRORED SEQUENCES

   457 <210> SEQ ID NO: 7
   458 <211> LENGTH: 309
   459 <212> TYPE: PRT
   460 <213> ORGANISM: bovine leukemia virus
   462 <400> SEQUENCE: 7
   464 Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys
E--> 465 1      5   10  5  15                  10              15       *[handwritten: see p. 2]*
   467 Pro Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys
E--> 468      20   25   30
   470 Pro Leu Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp
E--> 471      35   40   45                                           *[handwritten: misaligned]*
   473 Thr Thr His Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp   *[handwritten: amino acid]*
E--> 474      50   55   60                                           *[handwritten: numbers]*
   476 Gly Arg Pro Phe Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His
E--> 477      65   70   75                                           *[handwritten: (see item 3 on]*
   479 Val Ser Arg Asp Pro Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn  *[handwritten: Error Summary]*
E--> 480      80   85   90                                           *[handwritten: Sheet)]*
   482 Cys Pro Leu Pro Ala Val Arg Ala Gln Pro Gly Pro Val Ser Leu
E--> 483      95   100  105
   485 Ser Pro Phe Glu Arg Ser Pro Phe Gln Pro Tyr Gln Cys Gln Leu
E--> 486      110  115  120
   488 Pro Ser Ala Ser Ser Asp Gly Cys Pro Val Ile Gly His Gly Leu
E--> 489      125  130  135
   491 Leu Pro Trp Asn Asn Leu Val Thr His Pro Cys Pro Arg Lys Val
E--> 492      140  145  150
   494 Leu Ile Leu Asn Gln Met Ala Asn Phe Ser Leu Leu Pro Pro Phe
E--> 495      155  160  165
   497 Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser Val Phe Ala Pro
E--> 498      170  175  180
   500 Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu Leu Thr Leu

RAW SEQUENCE LISTING                    DATE: 07/12/2004
PATENT APPLICATION:  US/10/763,976      TIME: 15:16:58

Input Set : **N:\FATIMA\10763976.txt**
Output Set: **N:\CRF4\07122004\J763976.raw**

```
E--> 501      185      190      195
     503 Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe Ser Pro
E--> 504      200      205      210
     506 Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro Pro
E--> 507      215      220      225
     509 Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
E--> 510      230      235      240
     512 Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser
E--> 513      245      250      255
     515 Pro Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln
E--> 516      260      265      270
     518 Arg Phe Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala
E--> 519      275      280      285
     521 Ser Arg Lys Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu
E--> 522      290      295      300
E--> 524 **Glu Asn Glu Trp Leu Ser Arg Leu Phe** (***)  *delete*
E--> 525      305
     571 <210> SEQ ID NO: 8
     572 <211> LENGTH: 353
     573 <212> TYPE: PRT
     574 <213> ORGANISM: human T-lymphotropic virus 1
     576 <400> SEQUENCE: 8
     579 Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr
E--> 580 1        5       10       15
     582 Pro Val Tyr Val Phe Gly Asp Cys Val Gln Gly Asp Trp Cys Pro
E--> 583       20       25       30
     585 Ile Ser Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu
E--> 586       35       40       45
     588 Leu Ala Thr Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp
E--> 589       50       55       60
     591 Gly Arg Val Ile Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu
E--> 592       65       70       75
     594 Pro Ser Phe Pro Thr Gln Arg Thr Ser Lys Thr Leu Lys Val Leu
E--> 595       80       85       90
     597 Thr Pro Pro Ile Thr His Thr Thr Pro Asn Ile Pro Pro Ser Phe
E--> 598       95      100      105
     600 Leu Gln Ala Met Arg Lys Tyr Ser Pro Phe Arg Asn Gly Tyr Met
E--> 601      110      115      120
     603 Glu Pro Thr Leu Gly Gln His Leu Pro Thr Leu Ser Phe Pro Asp
E--> 604      125      130      135
     606 Pro Gly Leu Arg Pro Gln Asn Leu Tyr Thr Leu Trp Gly Gly Ser
E--> 607      140      145      150
     609 Val Val Cys Met Tyr Leu Tyr Gln Leu Ser Pro Pro Ile Thr Trp
E--> 610      155      160      165
     612 Pro Leu Leu Pro His Val Ile Phe Cys His Pro Gly Gln Leu Gly
E--> 613      170      175      180
     615 Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu Glu Leu Leu
E--> 616      185      190      195
     618 Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu Pro Glu
```

*(handwritten margin notes:)* same
This misalignment also occurs in sequences 2, 3, and 6

*(handwritten margin notes:)* misaligned amino acid numbers

RAW SEQUENCE LISTING          DATE: 07/12/2004
PATENT APPLICATION:  US/10/763,976          TIME: 15:16:58

Input Set : N:\FATIMA\10763976.txt
Output Set: N:\CRF4\07122004\J763976.raw

```
E--> 619        200    205       210
     621 Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro Val
E--> 622        215    220       225
     624 Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr
E--> 625        230    235       240
     627 Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro
E--> 628        245    250       255
     630 Met Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val
E--> 631        260    265       270
     633 Leu Gln Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala
E--> 634        275    280       285
     636 Tyr His Pro Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser
E--> 637        290    295       300
     639 Ser Phe His Asn Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile
E--> 640        305    310       315
     642 Pro Ile Ser Leu Leu Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp
E--> 643        320    325       330
     645 His Glu Pro Gln Ile Ser Pro Gly Gly Leu Glu Pro Pro Ser Glu
E--> 646        335    340       345
E--> 648 Lys His Phe Arg Glu Thr Glu Val (***)
E--> 649        350
     685 <210> SEQ ID NO: 9
     686 <211> LENGTH: 101
     687 <212> TYPE: PRT
     688 <213> ORGANISM: human immunodeficiency virus 1
     690 <400> SEQUENCE: 9
     692 Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly
E--> 693 1      5     10        15
     695 Ser Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys
E--> 696        20    25        30
     698 Cys Phe His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile
E--> 699        35    40        45
     701 Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln
E--> 702        50    55        60
     704 Asp Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser
E--> 705        65    70        75
     707 Gln Ser Arg Gly Asp Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys
E--> 708        80    85        90
E--> 710 Val Glu Arg Glu Thr Glu Thr Asp Pro Phe Asp (***)
E--> 711        95    100
```

*same*

*same*

*same*

*see p. 4 for more error*

```
<210> 1
<211> 576
<212> DNA
<213> Artificial Sequence

<220>
<221> Promoter
<222> 87..432
<223> BLV Promoter

<220>
<221> misc_feature
<222> 452..576
<223> attR1 Gateway recombination site

<400> 1
```

*This needs Explanation in <220>-<223> section.*

*Give source of genetic material.*

IMPORTANT

**The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.**

*Also, change all nucleotides from upper-case letters to lower-case letters*

*Since the Sequence Listing is in "new" Sequence Rules format, use lower-case letters for nucleotides.*

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:69 M:112 C: (48) String data converted to lower case,
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
M:112 Repeated in SeqNo=2
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:183 M:112 C: (48) String data converted to lower case,
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:112 Repeated in SeqNo=3
L:189 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:201 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:225 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:233 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:257 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

```
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:297 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=4
L:354 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=5
L:411 M:112 C: (48) String data converted to lower case,
L:413 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
M:112 Repeated in SeqNo=6
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:421 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:425 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:429 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:465 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:524 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:525 M:252 E: No. of Seq. differs, <211> LENGTH:Input:309 Found:310 SEQ:7
L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
M:342 Repeated in SeqNo=8
L:649 M:252 E: No. of Seq. differs, <211> LENGTH:Input:353 Found:354 SEQ:8
L:693 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
M:342 Repeated in SeqNo=9
L:711 M:252 E: No. of Seq. differs, <211> LENGTH:Input:101 Found:102 SEQ:9
L:795 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:1189 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=11
L:1530 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12
L:1872 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=13
```